

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:19:59 ; Search time 5588.75 Seconds
(without alignments)
11622.905 Million cell updates/sec

Title: US-09-625-573-1

Perfect score: 2232

Sequence: 1 GGATGAACAAGGACGCATT.....TATAACTATGTGTGATAAAG 2232

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2232	100.0	2232	6	AR116074	AR116074 Sequence
2	2232	100.0	2232	6	I79542	I79542 Sequence 1
3	2232	100.0	2232	6	HSU03882	U03882 Human monoc
4	1254	56.2	5471	9	HSU03882	U03882 Human monoc
5	1250.8	56.0	143068	6	AX335952	AX335952 Sequence
6	1250.8	56.0	143068	9	HSU05626	U05626 Homo sapien
7	1249.2	56.0	185437	9	AC098613	AC098613 Homo sapi
8	1068	47.8	1068	11	G07239	G07239 human STS W
9	980	43.9	1979	6	AR116075	AR116075 Sequence
10	980	43.9	1979	6	I79543	I79543 Sequence 3
11	980	43.9	1979	9	HSU03905	U03905 Human monoc
12	941	42.2	1083	6	AX232508	AX232508 Sequence
13	939.4	42.1	1083	6	AX232506	AX232506 Sequence
14	937.8	42.0	1083	6	HUWCP1R	D2984 Human mRNA
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16	897.8	39.9	1083	6	E13909	E13909 cDNA encodi
17	889.8	39.9	1083	9	AF013958	AF013958 Macaca mu
18	816.6	36.6	2900	2	AC087602	AC087602 Pan trogl
19	672.8	30.1	1365	10	RNU77349	U77349 Rattus norv
20	668.6	30.0	1364	10	MMU51717	U51717 Mus musculu
21	668.2	29.9	10528	6	AX345237	AX345237 Sequence
22	665.4	29.8	2992	10	MMU56819	U56819 Mus musculu
23	663.8	29.7	1245	10	MMU47035	U47035 Mus musculu
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27	643.6	28.8	1019	9	AF162029	AF162029 Cercopith
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ALIGNMENTS

RESULT 1
AR116074
LOCUS AR116074 2232 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6132987.
ACCESSION AR116074
VERSION AR116074.1 GI:14096396
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2232)
AUTHORS Charo, I.F. and Coughlin, S.R.
TITLE Recombinant mammalian monocyte chemotactic protein-1 (MCP-1)
receptors (MCP-1R, CCR-2)
JOURNAL Patent: US 6132987-A 1 17-OCT-2000;

FEATURES		Location/Qualifiers
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ORIGIN	/organism="unknown"	
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Best Local Similarity	100.0%;	Pred. No. 0;
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	0; Gaps	0;
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Db	661	ATTTTGGGGTGGTCCGCTGCTCATCATGGTCACTGCTACTCGGGAAATCCTGAAA 720
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Db	901	CAGGTGACAGAGACTCTTGGGATGACTCTACTGCTGCATCAATCCCATCATCTATGCCTTC 960

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DEFINITION	Sequence 1 from patent US 5707815.		
ACCESSION	I79542		
VERSION	I79542.1	GI:3207832	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2232)		
TITLE	Charo, I.F. and Coughlin, S.R.		
JOURNAL	Mammalian monocyte chemoattractant protein receptors and assays using them		
FEATURES	Patent: US 5707815-A 1 13-JAN-1998;		
	Location/Qualifiers		
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	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 2232; Conservative 0; Mismatches 0; Indels 0; Gaps		
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Db	1	GGATTGAACAAAGACGCAATTTCCCAAGTACATCCACACACATGCTGTCCACATCTCGTTCT	60
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RESULT 3
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LOCUS Human monocyte chemoattractant protein 1 receptor (MCP-1RA)
DEFINITION alternatively spliced mRNA, complete cds.
ACCESSION U03882
VERSION U03882.1 GI:472555
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2232)
AUTHORS Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and
Coughlin, S.R.
TITLE Molecular cloning and functional expression of two monocyte
chemoattractant protein 1 receptors reveals alternative splicing of
the carboxyl-terminal tails
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
MEDLINE 94195821
PUBMED 8146186
REFERENCE 2 (bases 1 to 2232)
AUTHORS Myers, S.J.
TITLE Direct Submission
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JOURNAL Submitted (01-DEC-1993) Scott J. Myers, Cardiovascular, The
USA Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110,
USA
FEATURES
source Location/Qualifiers
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BASE COUNT 602 a 464 c 508 g 658 t
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Best Local Similarity 100.0%; Pred. No. 0;
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Db 361 TTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCATCGGTATTTTGGCGGA 420
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Query Match 56.2%; Score 1254; DB 9; Length 5471; Best Local Similarity 100.0%; Pred. No. 0; Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 979 AGCCTTTTTCATAGCTCTTGGCTGTAGAGTTGCCCTCAAAACCCAGTGTGGA 1038 DB 3754 ACCCTTTTTCATAGCTCTTGGCTGTAGAGTTGCCCTCAAAACCCAGTGTGGA 3813 QY 1039 GGTCCAGGAGTGAGACAGAAAGATGTGAAGTCACTACCAAGAGCTCTTCGATGGT 1098 DB 3814 GGTCCAGGAGTGAGACAGAAAGATGTGAAGTCACTACCAAGAGCTCTTCGATGGT 3873 QY 1099 CGTGAAAAGGAAAGTCAATGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGGA 1158 DB 3874 CGTGAAAAGGAAAGTCAATGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGGA 3933 QY 1159 GCCTAGACAGAAATGACAGATCTCTGTTTGGAAATACACAGCTGCTTCACAGATG 1218 DB 3934 GCCTAGACAGAAATGACAGATCTCTGTTTGGAAATACACAGCTGCTTCACAGATG 3993 QY 1219 TGTGATTCACAGTGTGAATCTTGTGTCTACGTTACCGAGGAGGAGCTGAGAGAGAG 1278 DB 3994 TGTGATTCACAGTGTGAATCTTGTGTCTACGTTACCGAGGAGGAGCTGAGAGAGAG 4053 QY 1279 AGACTCCAGCTGGGTGAAAACAGATATTTCCAACTACCTTCCAGTTCCTCATTTTG 1338 DB 4054 AGACTCCAGCTGGGTGAAAACAGATATTTCCAACTACCTTCCAGTTCCTCATTTTG 4113 QY 1339 AATACAGCATAGAGTTCAGACTTTTTTAAATAGTAAATAAATAAAGCTGAAAC 1398 DB 4114 AATACAGCATAGAGTTCAGACTTTTTTAAATAGTAAATAAATAAAGCTGAAAC 4173 QY 1399 TGCACCTGTAAATGTGGTAAAGAGTGTAGTTGAGTGTCTATCATGTCAAAAGCTGAAAT 1458 DB 4174 TGCACCTGTAAATGTGGTAAAGAGTGTAGTTGAGTGTCTATCATGTCAAAAGCTGAAAT 4233 QY 1459 GCTGTATTAGTCACAGAGATAATTCTAGCTTTGAGCTTTAGCTTTAGAGCTTAAGAAATTTGAGCAGGTTGAT 1518

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RESULT 5 AX335952 143068 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 6461 from Patent WO0194629.
DEFINITION AX335952
ACCESSION AX335952.1 GI:18126671
VERSION AX335952.1
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G., Horrigan, S., Soppet, D. R., and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 6461 13-DEC-2001;
FEATURES Avalon Pharmaceuticals (US)
Location/Qualifiers 1. .143068
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NUMBER 0000247 / 68

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Number U80924), two alternatively spliced

Number U80924), two alternatively spliced mRNAs."

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AC098613	AC098613.2	GI:22038607
HTG.		
human.		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		
and Haugen, E.D.		
Direct Submission		
Unpublished		
2 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
Direct Submission		
Submitted (26-OCT-2001) Genome Center, University of Washington,		
Box 352145, Seattle, WA 98195, USA		
3 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		
and Haugen, E.D.		
Direct Submission		
Submitted (01-AUG-2002) Genome Center, University of Washington,		
Box 352145, Seattle, WA 98195, USA		
On Aug 1, 2002 this sequence version replaced gi:16445164.		

Center: University of Washington Genome Center		
Center Code: UWGC		
Web site: http://www.genome.washington.edu		
Contact: uwgchgs@u.washington.edu		

Project Information		

Center project name: chr-3		
Center clone name: RP11-24F11 (bc0137)		

Summary Statistics		

Sequencing vector: plasmid; L08752; 100% of reads		
Chemistry: Dye-terminator ET; 93% of reads		
Chemistry: Dye-terminator Big Dye; 7% of reads		
Assembly program: Phrap; version 0.990319		
Consensus quality: 184860 bases at least Q40		
Consensus quality: 185398 bases at least Q30		
Consensus quality: 185435 bases at least Q20		
Insert size: 185437; sum-of-contigs		
Quality coverage: 7.6x in Q20 bases; sum-of-contigs		

Overlapping Sequences:		
5': BAC-110P12 U95626, 11014-bp overlap		
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap		

Sequence Quality Assessment:		
This entry has been annotated with sequence quality		
estimates computed by the Phrap assembly program.		
All manually edited bases have been reduced to quality zero.		
Quality levels above 40 are expected to have less than		
1 error in 10,000 bp.		
Base-by-base quality values are not generally visible from the		
Genbank flat file format but are available as part		
of this entry's ASN.1 file.		

This sequence was finished as follows unless otherwise noted:		
all regions were either double-stranded or sequenced with an		
alternate chemistry or covered by high quality data (i.e., Phred		
quality >= 30); an attempt was made to resolve all sequencing		
problems, such as compressions and repeats; all regions were		
covered by at least one plasmid subclone or more than one M13		
subclone; and the assembly was confirmed by restriction digest.		

Sequence Validation:		
This sequence has been validated by Multiple Complete Digest		
fingerprinting. Comparison of the experimentally derived digest		
fragments with sequence-predicted fragments is given below.		
The electronically-digested sequence consists of both insert and		
vector, in order to accurately represent the entire circular BAC		

AC098613	AC098613.2	GI:22038607
HTG.		
human.		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		
and Haugen, E.D.		
Direct Submission		
Unpublished		
2 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
Direct Submission		
Submitted (26-OCT-2001) Genome Center, University of Washington,		
Box 352145, Seattle, WA 98195, USA		
3 (bases 1 to 185437)		
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		
and Haugen, E.D.		
Direct Submission		
Submitted (01-AUG-2002) Genome Center, University of Washington,		
Box 352145, Seattle, WA 98195, USA		
On Aug 1, 2002 this sequence version replaced gi:16445164.		

Center: University of Washington Genome Center		
Center Code: UWGC		
Web site: http://www.genome.washington.edu		
Contact: uwgchgs@u.washington.edu		

Project Information		

Center project name: chr-3		
Center clone name: RP11-24F11 (bc0137)		

Summary Statistics		

Sequencing vector: plasmid; L08752; 100% of reads		
Chemistry: Dye-terminator ET; 93% of reads		
Chemistry: Dye-terminator Big Dye; 7% of reads		
Assembly program: Phrap; version 0.990319		
Consensus quality: 184860 bases at least Q40		
Consensus quality: 185398 bases at least Q30		
Consensus quality: 185435 bases at least Q20		
Insert size: 185437; sum-of-contigs		
Quality coverage: 7.6x in Q20 bases; sum-of-contigs		

Overlapping Sequences:		
5': BAC-110P12 U95626, 11014-bp overlap		
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap		

Sequence Quality Assessment:		
This entry has been annotated with sequence quality		
estimates computed by the Phrap assembly program.		
All manually edited bases have been reduced to quality zero.		
Quality levels above 40 are expected to have less than		
1 error in 10,000 bp.		
Base-by-base quality values are not generally visible from the		
Genbank flat file format but are available as part		
of this entry's ASN.1 file.		

This sequence was finished as follows unless otherwise noted:		
all regions were either double-stranded or sequenced with an		
alternate chemistry or covered by high quality data (i.e., Phred		
quality &		

RESULT 7				
AC098613	AC098613	185437 bp	DNA	linear PRI 01-AUG-2002
LOCUS				
DEFINITION	Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.			

Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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5844	5720	3049	3078	3985	3998		
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13024	13045	13685	13328	435	<800		
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primer; sequence tagged site.
 Derived from sequences in dbEST and the Unigene
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Primates; Catarrhini; Hominidae; Homo.
)
 /MIT Center for Genome Research; Physically

Db 121 CAGCTGGGTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCTCTCATTTTGAATACA 180

DEFINITION human STS WI-9314, sequence tagged site.

AUTHORS	Charo, I.F. and Coughlin, S.R.
TITLE	Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)
JOURNAL	Patent: US 6132987-A 3 17-OCT-2000;
FEATURES	Location/Qualifiers
source	1..1979
BASE COUNT	530 a 435 c 451 g 563 t
ORIGIN	
Query Match	43.9%; Score 980; DB 6; Length 1979;
Best Local Similarity	100.0%; Pred. No. 7.9e-250;
Matches 980; Conservative	0; Mismatches 0; Indels 0; Gaps
QY 1	GGATTGAACAAGGACGCAATTTCCCCAGTAGTACATCCACAACATGCTGCCACATCTCGTTCT 605
Db	42 GGATTGAACAAGGACGCAATTTCCCCAGTACATCCACAACATGCTGCCACATCTCGTTCT 1010
QY 61	CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTACCACCTTTTTTGATTATGAT 121
Db	102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTACCACCTTTTTTGATTATGAT 161
QY 121	TACGGTGTCCCTGTGCATAAATTTACAGTGAAGCAAAATGGGGCCCACTCTCGCTCGG 18
Db	162 TACGGTGTCCCTGTGCATAAATTTACAGTGAAGCAAAATGGGGCCCACTCTCGCTCGG 22
QY 181	CTCTACTCGCTGGTGTTCATCTTTGGTTTTGGGCAACATGCTGGTGGTCTCATCTTA 24
Db	222 CTCTACTCGCTGGTGTTCATCTTTGGTTTTGGGCAACATGCTGGTGGTCTCATCTTA 28
QY 241	ATAAAGTCAAAAAGCTGAAGTGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 30
Db	282 ATAAAGTCAAAAAGCTGAAGTGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 34
QY 301	GATCTGCTTTTCTTATTACTCTCCATFTGGGCTCACTGCTGCAAAATGAGTGGGTC 36
Db	342 GATCTGCTTTTCTTATTACTCTCCATFTGGGCTCACTGCTGCAAAATGAGTGGGTC 40
QY 361	TTTGGGAATGCAATGTGCAAAATTTACACAGGGCTGTATCATATCGTATTTTGGCGGA 42
Db	402 TTTGGGAATGCAATGTGCAAAATTTACACAGGGCTGTATCATATCGTATTTTGGCGGA 46
QY 421	ATCTTCTTCATCATCTCTCGAATCGATAGATACCTGGCTATFTGTCATGCTGTGTT 48
Db	462 ATCTTCTTCATCATCTCTCGAATCGATAGATACCTGGCTATFTGTCATGCTGTGTT 52
QY 481	GCTTTAAAGCCAGGACGGTCACTTTGGGCTGGTACAGTGTGATCACCTGGTGGTG 54
Db	522 GCTTTAAAGCCAGGACGGTCACTTTGGGCTGGTACAGTGTGATCACCTGGTGGTG 58
QY 541	GCTGTGTTTGGTCTGTCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATCTCGTT 60
Db	582 GCTGTGTTTGGTCTGTCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATCTCGTT 64
QY 601	TATGTCTGTGGCCCTTATTTTCCACGAGATGGAATTAATTCACACAATATGAGGAAC 66
Db	642 TATGTCTGTGGCCCTTATTTTCCACGAGATGGAATTAATTCACACAATATGAGGAAC 70
QY 661	ATTTTGGGCTGTCTGCGCTGTCTATCATGTGATCTGCTACTCGGGAATCCTGAAA 72
Db	702 ATTTTGGGCTGTCTGCGCTGTCTATCATGTGATCTGCTACTCGGGAATCCTGAAA 76
QY 721	ACCTGCTTCGGTGTGCGAAGCAGAGAGAGGCATAGGCGAGTGAAGATCATCTTCAC 78
Db	762 ACCTGCTTCGGTGTGCGAAGCAGAGAGAGGCATAGGCGAGTGAAGATCATCTTCAC 82
QY 781	ATCATGATGTTTACTTTCTTCTTGACTCCCTATAACATTTGTCATTTCTCTGAACACC 84
Db	822 ATCATGATGTTTACTTTCTTCTTGACTCCCTATAACATTTGTCATTTCTCTGAACACC 88
QY 841	TTCCAGGAATCTTCGCGCTGAGTAACCTGTGAACGACCATGTAACACTGACCAAGCCACG 90
Db	882 TTCCAGGAATCTTCGCGCTGAGTAACCTGTGAACGACCATGTAACACTGACCAAGCCACG 94

Db	702	ATTTTGGGGCTGGTCTCTGCGGCTGCTCATCATGGTCATCTGCTACTCGGGAACTCTGAA	761
QY	721	ACCGTCTTTCGGTGTGCGAAGCAGAGAAGAGGCATAGGCGAGTAGAGAGTCACTTTCAAC	780
Db	762	ACCGTCTTTCGGTGTGCGAAGCAGAGAAGAGGCATAGGCGAGTAGAGAGTCACTTTCAAC	821
QY	781	ATCATGATTGTTTACTTCTCTTCCTGGACTCCCTATACATTGTCTATTCTCTCGAACACC	840
Db	822	ATCATGATTGTTTACTTCTCTTCCTGGACTCCCTATAACATTGTCTATTCTCTCGAACACC	881
QY	841	TTCCAGGAATTTCTCGGCTGAGTAACCTGTGAAAGCACCAGTCACTGGACCAAGCCAG	900
Db	882	TTCCAGGAATTTCTCGGCTGAGTAACCTGTGAAAGCACCAGTCACTGGACCAAGCCAG	941

/translation="MLSTSRSRFRIRNTNESGEVETTFDYDYGAPCHKFDVKQIGAOI
LPYLSLVFIFGFGVGNLVYLLINCKKLKLTIDYLLNLAIHVAIFLLITLPIWAHSA
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SVITLWVAVFASVPGIIFTKCKOKEDSVYVCGPFPGRWNNEPHITLRLNIGLVLLIM
VICYSGILKTLRLCRNEKKRHRVAVFTIMVYFLFWTPYINIVILINTFOEFFGLSN
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FRETVDGVSTNPSTPSTGEQEVSAGL"
BASE COUNT 530 a 435 c 451 g 563 t
ORIGIN

Query Match 43.9%; Score 980; DB 9; Length 1979;
Best Local Similarity 100.0%; Pred. No. 7.9e-250;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAGAGCGATTTCCCGAGTACATCCACAAATGCGTCCACATCTCGTTCT 60
DB 42 GGATTGAACAGAGCGATTTCCCGAGTACATCCACAAATGCGTCCACATCTCGTTCT 101
QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTACCACCTTTTGTGATTATGAT 120
DB 102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTACCACCTTTTGTGATTATGAT 161
QY 121 TAGGTTGCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGGGCCCCCAACTCCGCTCCG 180
DB 162 TAGGTTGCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGGGCCCCCAACTCCGCTCCG 221
QY 181 CTCTACTCGCTGGTGTCTCTTTGGTTTGGGGCAACATGCTGGTCTCATCTTA 240
DB 222 CTCTACTCGCTGGTGTCTCTTTGGTTTGGGGCAACATGCTGGTCTCATCTTA 281
QY 241 ATAACTGCAAAAGCTGAAGTCTTGACTGACATTTACTGCTCAACCTGGCCATCTCT 300
DB 282 ATAACTGCAAAAGCTGAAGTCTTGACTGACATTTACTGCTCAACCTGGCCATCTCT 341
QY 301 GATCTGCTTTTCTTACTCTCCATTTGGGCTCACTCTGCTGCAATGAGTGGTC 360
DB 342 GATCTGCTTTTCTTACTCTCCATTTGGGCTCACTCTGCTGCAATGAGTGGTC 401
QY 361 TTTGGGAATGCAATGTGCAAAATTTTACAGGCTGTATACATCGTTTATTTGGCGGA 420
DB 402 TTTGGGAATGCAATGTGCAAAATTTTACAGGCTGTATACATCGTTTATTTGGCGGA 461
QY 421 ATCTCTTCATCATCTCTGCAATGATAGATACCTGGCTATTGCTCATGCTGTGTTT 480
DB 462 ATCTCTTCATCATCTCTGCAATGATAGATACCTGGCTATTGCTCATGCTGTGTTT 521
QY 481 GCTTTAAAGCCAGGAGCTCACCTTTGGGTTGGTGAAGTGTGATCACTGGTGGTG 540
DB 522 GCTTTAAAGCCAGGAGCTCACCTTTGGGTTGGTGAAGTGTGATCACTGGTGGTG 581
QY 541 GCTGTTTGTCTGCTCCAGGAATCATCTTTACTAAATGCGCAGAAAGATTTCTGTT 600
DB 582 GCTGTTTGTCTGCTCCAGGAATCATCTTTACTAAATGCGCAGAAAGATTTCTGTT 641
QY 601 TATGCTGTGGCCCTTATTTCCAGGAGGATGGAATAATTTCCACAAATATGAGGAAC 660
DB 642 TATGCTGTGGCCCTTATTTCCAGGAGGATGGAATAATTTCCACAAATATGAGGAAC 701
QY 661 ATTTGGGGGTGGTCTGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 702 ATTTGGGGGTGGTCTGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
QY 721 ACCCTGCTCGGTGTCGAAACGAGAAGAGGATAGGGGAGTGAAGTCACTTTCACC 780
DB 762 ACCCTGCTCGGTGTCGAAACGAGAAGAGGATAGGGGAGTGAAGTCACTTTCACC 821
QY 781 ATCATGATTGTTTACTTCTTCTGAGTCCCTTATTAACATTTGATCTCTGCTGAGAAC 840
DB 822 ATCATGATTGTTTACTTCTTCTGAGTCCCTTATTAACATTTGATCTCTGCTGAGAAC 881
QY 841 TTCCAGGAATTTCTGGCCCTGAGTAACTGTGAAGACCACTGCACTGAGGACCCACG 900
DB 882 TTCCAGGAATTTCTGGCCCTGAGTAACTGTGAAGACCACTGCACTGAGGACCCACG 941

QY 901 CAGGTGACAGAGACTCTTGGGAGTCACTGCTGCTCAATCCATCATCTATGCTTC 960
DB 942 CAGGTGACAGAGACTCTTGGGAGTCACTGCTGCTCAATCCATCATCTATGCTTC 1001
QY 961 GTTGGGAGAGTTCAGAAG 980
DB 1002 GTTGGGAGAGTTCAGAAG 1021

RESULT 12
AX232508
LOCUS AX232508 1083 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 3 from Patent WO0162796.
ACCESSION AX232508
VERSION AX232508.1 GI:15592570

KEYWORDS
SOURCE human.

ORGANISM

Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1083)

TITLE Valdes, A.M., Groot, P.H. and Spurr, N.K.
Ccr2-64i, polymorphic variant of the human ccr2 receptor and its
use in the diagnostic and treatment of atherosclerosis

JOURNAL Patent: WO 0162796-A 3 30-AUG-2001;
SMITHKLINE BEECHAM PLC (GB)

FEATURES

Location/Qualifiers
1..1083

source

BASE COUNT 255 a 260 c 247 g 321 t

ORIGIN

Query Match 42.2%; Score 941; DB 6; Length 1083;

Best Local Similarity 100.0%; Pred. No. 1.9e-239;

Matches 941; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 ATGCTGTCCACATCTCGTCTCGTTTATCAGAAATACCAACGAGCGGTGAAGATC 99
DB 1 ATGCTGTCCACATCTCGTCTCGTTTATCAGAAATACCAACGAGCGGTGAAGATC 60
QY 100 ACCACCTTTTGTGATTATGATTACGGTCTCCCTGTCTATAAATTTGAGCTGAAGCAAT 159
DB 61 ACCACCTTTTGTGATTATGATTACGGTCTCCCTGTCTATAAATTTGAGCTGAAGCAAT 120
QY 160 GGGGCCCAACTCCCTCGCTCTACTCGTGTGTTTCATCTTTGTTGGGCAAC 219
DB 121 GGGGCCCAACTCCCTCGCTCTACTCGTGTGTTTCATCTTTGTTGGGCAAC 180
QY 220 ATGCTGTCTCTCATCTTTAAATAAAGCTGAAAAGCTGAAAGCTGACATTTAC 279
DB 181 ATGCTGTCTCTCATCTTTAAATAAAGCTGAAAAGCTGAAAGCTGACATTTAC 240
QY 280 CTGCTCAACTGGCCATCTGATCTCTTTTCTTACTCTCCATTTGGGCTCAC 339
DB 241 CTGCTCAACTGGCCATCTGATCTGCTTTTCTTACTCTCCATTTGGGCTCAC 300
QY 340 TCTGCTGCAAAATGAGTGGTCTTTGGGAATGCAATGCAATTTATTCACAGGCTGAT 399
DB 301 TCTGCTGCAAAATGAGTGGTCTTTGGGAATGCAATGCAATTTATTCACAGGCTGAT 360
QY 400 CACATCGGTTATTTGGCGGAATCTTCTTCATCATCTCTGCAATCGATAGACTG 459
DB 361 CACATCGGTTATTTGGCGGAATCTTCTTCATCATCTCTGCAATCGATAGACTG 420
QY 460 GCTATGTCATGCTGTTTGGTCTTTAAAGCCAGGAGCTCACTTTGGGCTGAT 519
DB 421 GCTATGTCATGCTGTTTGGTCTTTAAAGCCAGGAGCTCACTTTGGGCTGAT 480
QY 520 AGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 579
DB 481 AGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540

QY	580	TGCCAGAAAGAGATTCTGTTTATGCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT	639
Db	541	TGCCAGAAAGAGATTCTGTTTATGCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT	600
QY	640	TTCCACACAATAATGAGGACATTTTGGGCTGGTCCCTGCTCATCATGCTCATC	699
Db	601	TTCCACACAATAATGAGGACATTTTGGGCTGGTCCCTGCTCATCATGCTCATC	660
QY	700	TGCTACTCGGGAATCCTGAAACCCCTGCTTCGGTGTGCGAAAGAGAGGATAGG	759
Db	661	TGCTACTCGGGAATCCTGAAACCCCTGCTTCGGTGTGCGAAAGAGAGGATAGG	720
QY	760	GCAGTGAGAGTCATCTTCCACCATCATGATGTTTACTTCTCTTGGACTCCCTATAAC	819
Db	721	GCAGTGAGAGTCATCTTCCACCATCATGATGTTTACTTCTCTTGGACTCCCTATAAC	780
QY	820	ATTGTCATCTCTGAAACCTTCCAGGAATTTCTCGGCTCAGTAACCTGTGAAAGCACC	879
Db	781	ATTGTCATCTCTGAAACCTTCCAGGAATTTCTCGGCTCAGTAACCTGTGAAAGCACC	840
QY	880	AGTCAACTGGACCAAGCCAGGTCACAGAGACTTTGGGATGACTCACTGCTGCATC	939
Db	841	AGTCAACTGGACCAAGCCAGGTCACAGAGACTTTGGGATGACTCACTGCTGCATC	900
QY	940	AATCCCATCATCTATGCCCTTCGTTGGGGAGAGTTTCAGAG	980
Db	901	AATCCCATCATCTATGCCCTTCGTTGGGGAGAGTTTCAGAG	941
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LOCUS	AX232506	1083 bp	DNA linear PAT 11-SEP-2001
DEFINITION	Sequence 1 from Patent WO0162796.		
ACCESSION	AX232506		
VERSION	AX232506.1	GI:15592569	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1083)		
JOURNAL	Valdes, A.M., Groot, P.H. and Spurr, N.K.		
FEATURES	Ccr2-641, polymorphic variant of the human ccr2 receptor and its		
BASE COUNT	use in the diagnostic and treatment of atherosclerosis		
ORIGIN	Patent: WO 0162796-A 1 30-AUG-2001;		
	SMITHKLINE BEECHAM PLC (GB)		
	Location/Qualifiers		
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Best Local Similarity	99.9%	Pred. No. 5.1e-239;	
Matches 940;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	40	ATGCTGTCACATCTCGTTCCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTC	99
Db	1	ATGCTGTCACATCTCGTTCCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTC	60
QY	100	ACCACCTTTTGTGATTATGATTACGGTCTCCCTGTCATAAATTTGACGTGAAGCAAAAT	159
Db	61	ACCACCTTTTGTGATTATGATTACGGTCTCCCTGTCATAAATTTGACGTGAAGCAAAAT	120
QY	160	GGGGCCCAACTCCTGCCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTGGGCAAC	219
Db	121	GGGGCCCAACTCCTGCCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTGGGCAAC	180
QY	220	ATGCTGGTGGCTCCTCATCTTATAAAGCTGCAAAAGCTGACGTTCGACATTTAC	279
Db	181	ATGCTGGTGGCTCCTCATCTTATAAAGCTGCAAAAGCTGACGTTCGACATTTAC	240

QY	280	CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCATTTGGGCTCAC	339
Db	241	CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCATTTGGGCTCAC	300
QY	340	TCCTGCTCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTAT	399
Db	301	TCCTGCTCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTAT	360
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DEFINITION	Human mRNA for monocyte chemoattractant protein 1 receptor (MCP-1 receptor), complete cds.		
ACCESSION	D29984		
VERSION	D29984.1	GI:531246	
KEYWORDS	G-protein-coupled seven-transmembrane-type receptor; MCP-1 receptor; monocyte chemoattractant protein 1 receptor.		
SOURCE	Homo sapiens monocyte cell-line THP-1 cDNA to mRNA.		
ORGANISM	Homo sapiens		
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AUTHORS	1 (sites)		
TITLE	Yamagami, S., Tokuda, Y., Ishii, K., Tanaka, H. and Endo, N.		
JOURNAL	cDNA cloning and functional expression of a human monocyte		
MEDLINE	chemoattractant protein 1 receptor		
REFERENCE	Biochem. Biophys. Res. Commun. 202 (2), 1156-1162 (1994)		
JOURNAL	94324942		
REFERENCE	2 (bases 1 to 1083)		
AUTHORS	Yamagami, S.		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1083)		

AUTHORS Yamagami, S.
TITLE Direct Submission
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 Hino, Tokyo 191
 Japan
 Phone: 0425-86-8282
 Fax: 0425-87-5512.

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ACCESSION AX280849
VERSION AX280849.1 GI:16608180
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REFERENCE
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I. L.
TITLE Non-endogenous, constitutively activated known g protein-coupled
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JOURNAL Patent: WO 017172-A 472 18-OCT-2001;
 Arena Pharmaceuticals, Inc. (US)
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 Matches 939; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	580	TGCCAGAAAGAGATCTGTTTATGTCGTGGCCCTTATTTCCAGAGGATGGAATAAT	639
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Qy	640	TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCTGCTGCCGCTCATCATGTGTCATC	699
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Qy	880	AGTCAACTGGACCAAGCCAGGAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC	939
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